

CRF Errors Corrected by the STIC Systems Branch

CW

per/09

Serial Number: 09/830,837

CRF Processing Date: 2/26/2002  
 Edited by: [Signature]  
 Verified by: [Signature] (STIC staff)

**ENTERED**

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: \_\_\_\_\_
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☒ Other: Seqs 2,4,6 - corrected amino acid numbering

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.



PCT09

## RAW SEQUENCE LISTING

DATE: 02/26/2002

PATENT APPLICATION: US/09/830,837

TIME: 12:26:23

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02262002\I830837.raw

3 <110> APPLICANT: Institut de Recherches Cliniques de Montreal  
 4 SEIDAH, Nabil  
 5 CHRETIEN, Michel  
 6 MARCINKIEWICZ, Mieczyslaw  
 7 LAAKSONEN, Reijo  
 8 DAVIGNON, Jean  
 10 <120> TITLE OF INVENTION: MAMMALIAN SUBTILISIN/KEXIN ISOZYME SKI-1: A PROPROTEIN  
 11 CONVERTASE WITH A UNIQUE CLEAVAGE SPECIFICITY  
 13 <130> FILE REFERENCE: IRCM  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/09/830,837  
 C--> 16 <141> CURRENT FILING DATE: 2001-10-18  
 18 <150> PRIOR APPLICATION NUMBER: CA 2,249,648  
 19 <151> PRIOR FILING DATE: 1998-11-04  
 21 <160> NUMBER OF SEQ ID NOS: 76  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 3895  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Rattus sp.  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (418)..(3573)  
 34 <400> SEQUENCE: 1  
 35 gcgagtaa ac atccccgaa tggatacccg aggcgtgttc gcggcggagg ccccgttttc 60  
 37 ccgggtccgc cgatcccag cctgaggcga cgcagatcgg ctccagagcgg tggcttgggc 120  
 39 tctgtctaga tttgggtctg tggtaaaaat ggagtttagg actcagtga ctcggcccta 180  
 41 atgagagaag cccctgtcc aagatggaga agaagcggag aaagaaatga aagcctcttt 240  
 43 ttgggccaag ctgtgggtga ccatgggact gaggttttct ttacgttgga caagtctgta 300  
 45 ggatggctga tcagtaaggt tgcagctttt agcgaataca gaaatccact tctgatcaag 360  
 47 gaagagccta gtgcaatttg aatttatgca attttatgac catattcact taggacc 417  
 49 atg aag ctc gtc aac atc tgg ctt ctt ctg ctg gtg gtt ttg ctc tgt 465  
 50 Met Lys Leu Val Asn Ile Trp Leu Leu Leu Leu Val Val Leu Leu Cys  
 51 1 5 10 15  
 53 ggg aaa aag cat ctg ggt gac agg ctg ggg aag aaa gct ttt gaa aag 513  
 54 Gly Lys Lys His Leu Gly Asp Arg Leu Gly Lys Lys Ala Phe Glu Lys  
 55 20 25 30  
 57 gcc cca tgc ccc agc tgt tcc cac ctg act ttg aag gtg gaa ttc tcc 561  
 58 Ala Pro Cys Pro Ser Cys Ser His Leu Thr Leu Lys Val Glu Phe Ser  
 59 35 40 45  
 61 tca act gtg gtg gaa tat gaa tat att gtg gct ttc aac gga tac ttc 609  
 62 Ser Thr Val Val Glu Tyr Glu Tyr Ile Val Ala Phe Asn Gly Tyr Phe  
 63 50 55 60  
 65 aca gcc aaa gct aga aac tca ttt att tca agt gct cta aaa agc agt 657

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02262002\I830837.raw

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66 Thr Ala Lys Ala Arg Asn Ser Phe Ile Ser Ser Ala Leu Lys Ser Ser
67 65 70 75 80
69 gaa gtg gac aac tgg aga ata ata cct cgg aac aac cca tct agt gac 705
70 Glu Val Asp Asn Trp Arg Ile Ile Pro Arg Asn Asn Pro Ser Ser Asp
71 85 90 95
73 tac cct agt gat ttt gag gtg att cag ata aaa gag aag cag aag gcg 753
74 Tyr Pro Ser Asp Phe Glu Val Ile Gln Ile Lys Glu Lys Gln Lys Ala
75 100 105 110
77 ggg ctg ctc aca ctt gaa gat cac cca aac atc aag cgg gtg aca ccc 801
78 Gly Leu Leu Thr Leu Glu Asp His Pro Asn Ile Lys Arg Val Thr Pro
79 115 120 125
81 cag cgg aaa gtc ttt cgt tcc ctg aag ttt gct gaa tcc gac ccc att 849
82 Gln Arg Lys Val Phe Arg Ser Leu Lys Phe Ala Glu Ser Asp Pro Ile
83 130 135 140
85 gtg ccc tgt aat gag acc cgg tgg agc cag aag tgg cag tca tca cgt 897
86 Val Pro Cys Asn Glu Thr Arg Trp Ser Gln Lys Trp Gln Ser Ser Arg
87 145 150 155 160
89 ccc ctg aaa aga gcc agt ctc tcc ctg ggc tct gga ttc tgg cat gca 945
90 Pro Leu Lys Arg Ala Ser Leu Ser Leu Gly Ser Gly Phe Trp His Ala
91 165 170 175
93 aca gga agg cat tca agt cga cga ttg ctg aga gcc att cct cgc cag 993
94 Thr Gly Arg His Ser Ser Arg Arg Leu Leu Arg Ala Ile Pro Arg Gln
95 180 185 190
97 gtt gcc cag aca ttg cag gca gat gtg ctt tgg cag atg gga tac aca 1041
98 Val Ala Gln Thr Leu Gln Ala Asp Val Leu Trp Gln Met Gly Tyr Thr
99 195 200 205
101 ggt gct aat gtc agg gtt gcc gtt ttt gat act ggg ctc agt gag aag 1089
102 Gly Ala Asn Val Arg Val Ala Val Phe Asp Thr Gly Leu Ser Glu Lys
103 210 215 220
105 cat cca cat ttc aag aat gtg aag gaa aga acc aac tgg acc aat gag 1137
106 His Pro His Phe Lys Asn Val Lys Glu Arg Thr Asn Trp Thr Asn Glu
107 225 230 235 240
109 cgg acc ctg gac gat ggg ctg ggc cat ggc aca ttc gtt gca ggt gtg 1185
110 Arg Thr Leu Asp Asp Gly Leu Gly His Gly Thr Phe Val Ala Gly Val
111 245 250 255
113 att gcc agc atg aga gag tgc caa gga ttt gcc cca gat gca gag ctg 1233
114 Ile Ala Ser Met Arg Glu Cys Gln Gly Phe Ala Pro Asp Ala Glu Leu
115 260 265 270
117 cac atc ttc agg gtc ttt acc aac aat cag gtg tct tac acg tct tgg 1281
118 His Ile Phe Arg Val Phe Thr Asn Asn Gln Val Ser Tyr Thr Ser Trp
119 275 280 285
121 ttt ttg gat gcc ttc aac tat gcc atc cta aag aag atg gac gtt ctg 1329
122 Phe Leu Asp Ala Phe Asn Tyr Ala Ile Leu Lys Lys Met Asp Val Leu
123 290 295 300
125 aac ctt agc atc ggt ggg cct gac ttc atg gat cac ccc ttt gtt gac 1377
126 Asn Leu Ser Ile Gly Gly Pro Asp Phe Met Asp His Pro Phe Val Asp
127 305 310 315 320
129 aag gta tgg gaa tta aca gcg aac aat gta atc atg gtt tct gct att 1425
130 Lys Val Trp Glu Leu Thr Ala Asn Asn Val Ile Met Val Ser Ala Ile

```

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131		325		330		335		
133	ggc aat gat gga cct ctc tat ggc act ctg aat aac cct gct gat cag							1473
134	Gly Asn Asp Gly Pro Leu Tyr Gly Thr Leu Asn Asn Pro Ala Asp Gln							
135		340		345		350		
137	atg gat gtg att gga gtg ggt ggc att gac ttt gaa gac aac atc gcc							1521
138	Met Asp Val Ile Gly Val Gly Gly Ile Asp Phe Glu Asp Asn Ile Ala							
139		355		360		365		
141	cgc ttc tct tcc agg gga atg act acc tgg gaa cta ccg gga ggc tat							1569
142	Arg Phe Ser Ser Arg Gly Met Thr Thr Trp Glu Leu Pro Gly Gly Tyr							
143		370		375		380		
145	ggt cgt gtg aag cct gac att gtc acc tat ggt gct gga gtg cgg ggt							1617
146	Gly Arg Val Lys Pro Asp Ile Val Thr Tyr Gly Ala Gly Val Arg Gly							
147	385		390		395		400	
149	tct ggt gtg aaa ggg ggc tgc cgt gca ctc tca ggg acc agt gtc gcc							1665
150	Ser Gly Val Lys Gly Gly Cys Arg Ala Leu Ser Gly Thr Ser Val Ala							
151		405		410		415		
153	tcc cca gtg gtt gct ggg gct gtc acc ttg tta gta agc aca gta cag							1713
154	Ser Pro Val Val Ala Gly Ala Val Thr Leu Leu Val Ser Thr Val Gln							
155		420		425		430		
157	aag cgg gag cta gtg aat cct gcc agt gtg aag caa gct ttg ata gca							1761
158	Lys Arg Glu Leu Val Asn Pro Ala Ser Val Lys Gln Ala Leu Ile Ala							
159		435		440		445		
161	tca gcc cgg aga ctt cct ggt gtc aac atg ttt gag caa ggc cat ggc							1809
162	Ser Ala Arg Arg Leu Pro Gly Val Asn Met Phe Glu Gln Gly His Gly							
163		450		455		460		
165	aag ttg gat cta ctg cga gcc tat cag atc ctc agc agc tat aaa ccg							1857
166	Lys Leu Asp Leu Leu Arg Ala Tyr Gln Ile Leu Ser Ser Tyr Lys Pro							
167		465		470		475		480
169	cag gcg agc ctg agt cct agc tac atc gac ctg act gag tgt ccc tac							1905
170	Gln Ala Ser Leu Ser Pro Ser Tyr Ile Asp Leu Thr Glu Cys Pro Tyr							
171		485		490		495		
173	atg tgg ccc tac tgc tcc cag ccc atc tac tat gga gga atg cca aca							1953
174	Met Trp Pro Tyr Cys Ser Gln Pro Ile Tyr Tyr Gly Gly Met Pro Thr							
175		500		505		510		
177	att gtt aat gtc acc atc ctc aat ggc atg gga gtt aca gga aga att							2001
178	Ile Val Asn Val Thr Ile Leu Asn Gly Met Gly Val Thr Gly Arg Ile							
179		515		520		525		
181	gtg gat aag cct gag tgg cga ccc tat tta cca cag aat gga gac aac							2049
182	Val Asp Lys Pro Glu Trp Arg Pro Tyr Leu Pro Gln Asn Gly Asp Asn							
183		530		535		540		
185	att gaa gtg gcc ttc tcc tac tcc tca gtg ttg tgg cct tgg tca ggt							2097
186	Ile Glu Val Ala Phe Ser Tyr Ser Ser Val Leu Trp Pro Trp Ser Gly							
187		545		550		555		560
189	tac ctt gcc atc tcc att tct gtg acc aag aag gca gct tcc tgg gaa							2145
190	Tyr Leu Ala Ile Ser Ile Ser Val Thr Lys Lys Ala Ala Ser Trp Glu							
191		565		570		575		
193	ggc atc gcg cag ggc cac atc atg atc aca gtg gct tcc cca gca gag							2193
194	Gly Ile Ala Gln Gly His Ile Met Ile Thr Val Ala Ser Pro Ala Glu							
195		580		585		590		

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197	acg	gaa	tta	aaa	aat	ggt	gcc	gag	cat	act	tcc	aca	gtg	aag	ctg	ccc	2241
198	Thr	Glu	Leu	Lys	Asn	Gly	Ala	Glu	His	Thr	Ser	Thr	Val	Lys	Leu	Pro	
199			595				600					605					
201	atc	aag	gtg	aag	atc	att	ccc	acc	cct	cct	cgg	agc	aag	aga	gtc	ctc	2289
202	Ile	Lys	Val	Lys	Ile	Ile	Pro	Thr	Pro	Pro	Arg	Ser	Lys	Arg	Val	Leu	
203		610					615					620					
205	tgg	gac	cag	tac	cac	aac	ctc	cgc	tac	cca	ccc	ggc	tac	ttc	ccc	agg	2337
206	Trp	Asp	Gln	Tyr	His	Asn	Leu	Arg	Tyr	Pro	Pro	Gly	Tyr	Phe	Pro	Arg	
207	625					630				635						640	
209	gac	aac	ttg	cgg	atg	aag	aat	gat	cct	tta	gac	tgg	aat	ggc	gac	cac	2385
210	Asp	Asn	Leu	Arg	Met	Lys	Asn	Asp	Pro	Leu	Asp	Trp	Asn	Gly	Asp	His	
211					645				650					655			
213	gtc	cac	acc	aac	ttc	agg	gac	atg	tac	cag	cat	ctg	cgc	agc	atg	ggc	2433
214	Val	His	Thr	Asn	Phe	Arg	Asp	Met	Tyr	Gln	His	Leu	Arg	Ser	Met	Gly	
215				660					665					670			
217	tac	ttt	gtg	gag	gtg	ctt	ggt	gcc	cca	ttc	aca	tgc	ttt	gac	gcc	acg	2481
218	Tyr	Phe	Val	Glu	Val	Leu	Gly	Ala	Pro	Phe	Thr	Cys	Phe	Asp	Ala	Thr	
219				675				680						685			
221	cag	tac	ggc	act	ctg	ctt	atg	gtg	gac	agt	gag	gaa	gag	tac	ttc	cct	2529
222	Gln	Tyr	Gly	Thr	Leu	Leu	Met	Val	Asp	Ser	Glu	Glu	Glu	Tyr	Phe	Pro	
223		690					695					700					
225	gag	gag	att	gct	aag	ctg	agg	agg	gac	gtg	gac	aat	ggc	ctt	tcc	ctt	2577
226	Glu	Glu	Ile	Ala	Lys	Leu	Arg	Arg	Asp	Val	Asp	Asn	Gly	Leu	Ser	Leu	
227	705					710					715					720	
229	gtc	gtc	ttc	agt	gac	tgg	tac	aac	act	tct	gtt	atg	aga	aaa	gtg	aag	2625
230	Val	Val	Phe	Ser	Asp	Trp	Tyr	Asn	Thr	Ser	Val	Met	Arg	Lys	Val	Lys	
231					725					730					735		
233	ttt	tac	gat	gaa	aac	aca	agg	cag	tgg	tgg	atg	cca	gat	act	gga	gga	2673
234	Phe	Tyr	Asp	Glu	Asn	Thr	Arg	Gln	Trp	Trp	Met	Pro	Asp	Thr	Gly	Gly	
235				740					745					750			
237	gcc	aac	gtc	cca	gct	cta	aac	gag	ctg	ctg	tct	gtg	tgg	aac	atg	ggg	2721
238	Ala	Asn	Val	Pro	Ala	Leu	Asn	Glu	Leu	Leu	Ser	Val	Trp	Asn	Met	Gly	
239				755					760					765			
241	ttc	agt	gac	ggc	ctg	tat	gaa	ggg	gag	ttt	gcc	ctg	gca	aac	cac	gac	2769
242	Phe	Ser	Asp	Gly	Leu	Tyr	Glu	Gly	Glu	Phe	Ala	Leu	Ala	Asn	His	Asp	
243		770					775					780					
245	atg	tac	tat	gca	tcg	ggg	tgc	agc	att	gcc	agg	ttt	cca	gaa	gat	ggt	2817
246	Met	Tyr	Tyr	Ala	Ser	Gly	Cys	Ser	Ile	Ala	Arg	Phe	Pro	Glu	Asp	Gly	
247	785					790					795					800	
249	gtg	gtg	atc	aca	cag	act	ttc	aag	gac	caa	gga	ttg	gaa	gtc	tta	aaa	2865
250	Val	Val	Ile	Thr	Gln	Thr	Phe	Lys	Asp	Gln	Gly	Leu	Glu	Val	Leu	Lys	
251					805					810						815	
253	caa	gag	aca	gca	gtt	gtc	gac	aat	gtc	ccc	att	ctg	ggg	cta	tat	cag	2913
254	Gln	Glu	Thr	Ala	Val	Val	Asp	Asn	Val	Pro	Ile	Leu	Gly	Leu	Tyr	Gln	
255				820					825					830			
257	att	cca	gct	gaa	ggt	gga	ggc	cgg	att	gtg	ctg	tat	gga	gac	tcc	aac	2961
258	Ile	Pro	Ala	Glu	Gly	Gly	Gly	Arg	Ile	Val	Leu	Tyr	Gly	Asp	Ser	Asn	
259				835				840						845			
261	tgc	ttg	gat	gac	agt	cac	aga	cag	aag	gac	tgc	ttt	tgg	ctt	ctg	gat	3009

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Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02262002\I830837.raw

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262 Cys Leu Asp Asp Ser His Arg Gln Lys Asp Cys Phe Trp Leu Leu Asp
263      850      855      860
265 gca ctc ctt cag tac aca tcc tat ggt gtg acc cct ccc agc ctc agc 3057
266 Ala Leu Leu Gln Tyr Thr Ser Tyr Gly Val Thr Pro Pro Ser Leu Ser
267 865      870      875      880
269 cat tca ggg aac cgg cag cgc cca ccc agc ggg gct ggc ttg gcc cct 3105
270 His Ser Gly Asn Arg Gln Arg Pro Pro Ser Gly Ala Gly Leu Ala Pro
271      885      890      895
273 cct gaa agg atg gaa gga aac cac ctt cat cgc tac tcc aaa gtt ctt 3153
274 Pro Glu Arg Met Glu Gly Asn His Leu His Arg Tyr Ser Lys Val Leu
275      900      905      910
277 gag gcc cac ttg gga gac ccg aaa cct cgg ccc ctt cca gcc tgt cca 3201
278 Glu Ala His Leu Gly Asp Pro Lys Pro Arg Pro Leu Pro Ala Cys Pro
279      915      920      925
281 cac ttg tcg tgg gcc aag cca cag cct ttg aat gag acg gca ccc agt 3249
282 His Leu Ser Trp Ala Lys Pro Gln Pro Leu Asn Glu Thr Ala Pro Ser
283      930      935      940
285 aat ctt tgg aaa cac cag aag ctg ctc tcc att gac ctg gac aaa gta 3297
286 Asn Leu Trp Lys His Gln Lys Leu Leu Ser Ile Asp Leu Asp Lys Val
287 945      950      955      960
289 gtg tta ccc aac ttt cgc tca aat cgc cct caa gtg aga cct ttg tcc 3345
290 Val Leu Pro Asn Phe Arg Ser Asn Arg Pro Gln Val Arg Pro Leu Ser
291      965      970      975
293 cct gga gaa agt ggt gcc tgg gac att cct gga ggg atc atg cct ggc 3393
294 Pro Gly Glu Ser Gly Ala Trp Asp Ile Pro Gly Gly Ile Met Pro Gly
295      980      985      990
297 cgc tac aac cag gaa gta ggc cag acc atc cct gtt ttt gcc ttc ctt 3441
298 Arg Tyr Asn Gln Glu Val Gly Gln Thr Ile Pro Val Phe Ala Phe Leu
299      995      1000      1005
301 gga gcc atg gtg gcc ctg gcc ttc ttc gtg gta cag atc agt aag gcc 3489
302 Gly Ala Met Val Ala Leu Ala Phe Phe Val Val Gln Ile Ser Lys Ala
303      1010      1015      1020
305 aag agc cgg ccg aag cgg agg agg ccc agg gca aag cgt cca caa ctt 3537
306 Lys Ser Arg Pro Lys Arg Arg Arg Pro Arg Ala Lys Arg Pro Gln Leu
307 1025      1030      1035      1040
309 gca cag cag gcc cac cct gca agg acc ccg tca gtg tgatcatcac 3583
310 Ala Gln Gln Ala His Pro Ala Arg Thr Pro Ser Val
311      1045      1050
313 agtggccaga cacagaagct gacaagcttt gaacccctct ggtggccaca cagcatcaga 3643
315 gagcatcctg ggaagtgcct gtttccaagg agccctatct ctggattgtg gctggcttag 3703
317 tgtgttctgc ccagacgtct atgaggtaca tctgcagtg cctcactgtg tttggctctg 3763
319 gccgaagggtg cccagtagct cagcctccgg tggcatcagg cccagtgaca gtgcacaaaa 3823
321 gacacagagc ctggaagggc tgtcgggaca tactttctac ataatgctac aacctgacc 3883
323 aagcgaagac at 3895
326 <210> SEQ ID NO: 2
327 <211> LENGTH: 1052
328 <212> TYPE: PRT
329 <213> ORGANISM: Rattus sp.
331 <400> SEQUENCE: 2

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→ Use of n and/or Xaa has been detected in the Sequence Listing.  
Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/830,837

DATE: 02/26/2002

TIME: 12:26:24

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\02262002\I830837.raw

L:15 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:1586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:1625 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8  
L:1659 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9  
L:1698 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10  
L:1732 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11  
L:1771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12  
L:1807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:1846 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:1904 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:1926 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:1959 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:2292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:46  
L:2315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47  
L:2601 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74  
L:2624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75  
L:2647 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:76